

FIG. 1

FIGURE 1.
TRFP CHAIN 1, LEADER A

10	20	30	40	50	60
CTGCATCATGAAGGGGGCTCGTGTTCTCGTGCTTCTCTGGGCTGCCTTGCTCTTGATCTG					
C I M K G A R V L V L L W A A L L L I W					
70	80	90	100	110	120
GGGTGGAAATTGTGAAATTTGCCAGCCGTGAAGAGGGATGTTGACCTATTCCTGACGGG					
G G N C E I C P A V K R D V D L F L T G					
130	140	150	160	170	180
AACCCCGACGAATATGTTGAGCAAGTGGCACAATACAAAGCACTACCTGTAGTATTGGA					
T P D E Y V E Q V A Q Y K A L P V V L E					
190	200	210	220	230	240
AAATGCCAGAATACTGAAGAACTGCGTTGATGCAAAAATGACAGAAGAGGATAAGGAGAA					
N A R I L K N C V D A K M T E E D K E N					
250	260	270	280	290	300
TGCTCTCAGCTTGCTGGACAAAATATACACAAGTCCTCTGTGTTAAAGGAGCCATCACTG					
A L S L L D K I Y T S P L C -					
310	320	330	340	350	360
CCAGGAGCCCTAAGGAAGCCACTGAACTGATCACTAAGTAGTCTCAGCAGCCTGCCATGT					
370	380	390	400	410	
CCAGGTGTCTTACTAGAGGATTCCAGCAATAAAAGCCTGGCAATTCAAACAAAAAAA					

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FIG. 2

FIGURE 2.
TRFP CHAIN 1, LEADER B

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      10      20      30      40      50      60
      |      |      |      |      |      |
GGCCTGGCGGTGCTCCTGGAAAAGGATGTTAGACGCAGCCCTCCCACCCTGCCCTACTGT
  A  W  R  C  S  W  K  R  M  L  D  A  A  L  P  P  C  P  T  V

      70      80      90      100     110     120
      |      |      |      |      |      |
TGCGGCCACAGCAGATTGTGAAATTTGCCAGCCGTGAAGAGGGATGTTGACCTATTCCT
  A  A  T  A  D  C  E  I  C  P  A  V  K  R  D  V  D  L  F  L

      130     140     150     160     170     180
      |      |      |      |      |      |
GACGGGAACCCCGACGAATATGTTGAGCAAGTGGCACAATACAAAGCACTACCTGTAGT
  T  G  T  P  D  E  Y  V  E  Q  V  A  Q  Y  K  A  L  P  V  V

      190     200     210     220     230     240
      |      |      |      |      |      |
ATTGGAAAATGCCAGAATACTGAAGAACTGCGTTGATGCAAAAATGACAGAAGAGGATAA
  L  E  N  A  R  I  L  K  N  C  V  D  A  K  M  T  E  E  D  K

      250     260     270     280     290     300
      |      |      |      |      |      |
GGAGAATGCTCTCAGCTTGCTGGACAAAATATACACAAGTCCTCTGTGTTAAAGGAGCCA
  E  N  A  L  S  L  L  D  K  I  Y  T  S  P  L  C  -  R  S  H

      310     320     330     340     350     360
      |      |      |      |      |      |
TCACTGCCAGGAGCCCTAAGGAAGCCACTGAACTGATCACTAAGTAGTCTCAGCAGCCTG

      370     380     390     400     410     420
      |      |      |      |      |      |
CCATGTCCAGGTGTCTTACTAGAGGATTCCAGCAATAAAAGCCTTGCAATTCAAACAAAA
  
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FIG. 3

FIGURE 3.
TRFP CHAIN 2, LONG FORM

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      10      20      30      40      50      60
      |      |      |      |      |      |
TGACACGATGAGGGGGGCACTGCTTGTGCTGGCATTGCTGGTGACCCAAGCGCTGGGCGT
D T M R G A L L V L A L L V T Q A L G V

      70      80      90      100     110     120
      |      |      |      |      |      |
CAAGATGGCGGAAACTTGCCCCATTTTTATGACGTCCTTTTGGCGGTGGCCAATGGAAA
K M A E T C P I F Y D V F F A V A N G N

      130     140     150     160     170     180
      |      |      |      |      |      |
TGAATTACTGTTGGACTTGTCCCTCACAAAAGTCAATGCTACTGAACCAGAGAGAACAGC
E L L L D L S L T K V N A T E P E R T A

      190     200     210     220     230     240
      |      |      |      |      |      |
CATGAAAAAATCCAGGATTGCTACGTGGAGAACGGACTCATATCCAGGGTCTTGGATGG
M K K I Q D C Y V E N G L I S R V L D G

      250     260     270     280     290     300
      |      |      |      |      |      |
ACTAGTCATGACAACCATCAGCTCCAGCAAAGATTGCATGGGTGAAGCAGTTCAGAACAC
L V M T T I S S S K D C M G E A V Q N T

      310     320     330     340     350     360
      |      |      |      |      |      |
CGTAGAAGATCTCAAGCTGAACACTTTGGGGAGATGAATCTTTGCCACTGATGCCCCTTC
V E D L K L N T L G R -

      370     380     390     400     410     420
      |      |      |      |      |      |
TGAGCCCCATCCTCCTGCCCTGTTCTTTACACCTAAAGCTGGAATCCAGACACCTGTCCT

      430     440     450     460     470
      |      |      |      |      |
CACCTAATTCACTCTCAATCAGGCTGACTAGATAAAATAACTGCATCTTAAAAAA

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FIG. 4

FIGURE 4.
TRFP I CHAIN 2, SHORT FORM

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      10      20      30      40      50      60
      |      |      |      |      |      |
GACACGATGAGGGGGGCACTGCTTGTGCTGGCATTGCTGGTGACCCAAGCGCTGGGCGTC
D T M R G A L L V L A L L V T Q A L G V

      70      80      90      100     110     120
      |      |      |      |      |      |
AAGATGGCGGAGACGTGCCCCATTTTTTATGACGTCTTTTTTGCGGTGGCCAATGGAAAT
K M A E T C P I F Y D V F F A V A N G N

      130     140     150     160     170     180
      |      |      |      |      |      |
GAATTACTGTTGGACTTGTCCCTCACAAAAGTCAATGCTACTGAACCAGAGAGAACAGCC
E L L L D L S L T K V N A T E P E R T A

      190     200     210     220     230     240
      |      |      |      |      |      |
ATGAAAAAATCCAGGATTGCTACGTGGAGAACGGACTCATATCCAGGGTCTTGATGGA
M K K I Q D C Y V E N G L I S R V L D G

      250     260     270     280     290     300
      |      |      |      |      |      |
CTAGTCATGATAGCCATCAACGAATATTGCATGGGTGAAGCAGTTCAGAACACCGTAGAA
L V M I A I N E Y C M G E A V Q N T V E

      310     320     330     340     350     360
      |      |      |      |      |      |
GATCTCAAGCTGAACACTTTGGGGAGATGAATCTTTGCCACTGATGCCCCTTCTGAGCCC
D L K L N T L G R -

      370     380     390     400     410     420
      |      |      |      |      |      |
CATCCTCCTGTCCTGTTCTTTACACCTAAAGCTGGAATCCAGACACCTGTCCTCACCTAA

      430     440     450     460
      |      |      |      |
TTCACCTCTCAATCAGGCTGACTAGATAAAATAACTGCATCTTAAAAAA

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FIG. 5

FIGURE 5.
TRFP CHAIN 2, TRUNCATED SHORT FORM

10	20	30	40	50	60
GACACGATGAGGGGGGCACTGCTTGCTGCTGGCATTGCTGGTGACCCAAGCGCTGGGCGTC					
D T M R G A L L V L A L L V T Q A L G V					
70	80	90	100	110	120
AAGATGGCGGAGACGTGCCCCATTTTTTATGACGTCTTTTTTGCAGGTGGCCAATGGAAAT					
K M A E T C P I F Y D V F F A V A N G N					
130	140	150	160	170	180
GAATTACTGTTGGACTTGTCCTCACAAAAGTCAATGCTACTGAACCAGAGAGAACAGCC					
E L L L D L S L T K V N A T E P E R T A					
190	200	210	220	230	240
ATGAAAAAATCCAGGATTGCTACGTGGAGAACGGACTCATATCCAGGGTCTTGATGGA					
M K K I Q D C Y V E N G L I S R V L D G					
250	260	270	280	290	300
CTAGTCATGCCATCAACGAATATTGCATGGGTGAAGCAGTTCAGAACACCGTAGAAGATC					
L V M P S T N I A W V K Q F R T P -					
310	320	330	340	350	360
TCAAGCTGAACACTTTGGGGAGATGAATCTTTGCCACTGATGCCCCTTCTGAGCCCCATC					
370	380	390	400	410	420
CTCCTGTCCTGTTCTTTACACCTAAAGCTGGAATCCAGACACCTGTCCTCACCTAATTCA					
430	440	450	460		
CTCTCAATCAGGCTGACTAGATAAAATAACATGCATCTTAAAAAA					

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CI Leader A
-20
-10
C I M K G A R V L V L L W A A L L L I W G G N C

CI Leader B A W R C S W K R M L D A A L P P C P T B A A T A D C

```

      5   10   15   20   25   30   35
CICP AVKRDVDLFLTGTPDEYVEQV A Q Y K A L P V V L
PRO. - - - - - - - - - - - - - - - - - - - - -

```

	40	45	50	55	60	65	70
CI	E	N	A	R	I	L	K
	N	C	V	D	A	K	M
	T	E	E	D	K	E	N
	A	L	S	L	D	K	I
	Y	T	S	P	L	C	
PRO.							

FIG. 7

[illegible][illegible]

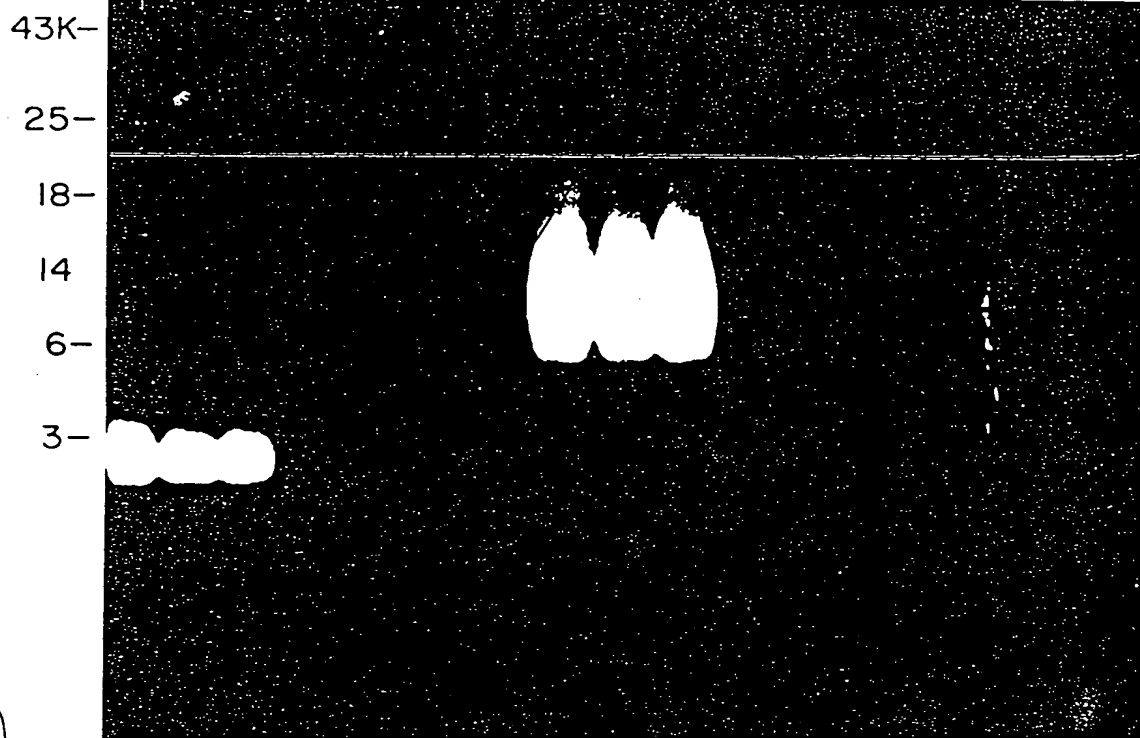
FIG. 7 (con't.)

	45	50	55	60	65	70	75	80
C2L	A M K K I Q D C Y V E N G L I S R V L D G L V M T T I S S S K D C M G E A V Q N							
C2S	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	I A - N E * * Y - - - - -	- - - - -	- - - - -
C2ST	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	P S T N I A W V K Q F R T P		
PRO.	- - - - -	- - - - -	- - - - -	- - - - -	T T - S S (K) - - - - -	I A - N E - - - - -	- - - - -	- - - - -

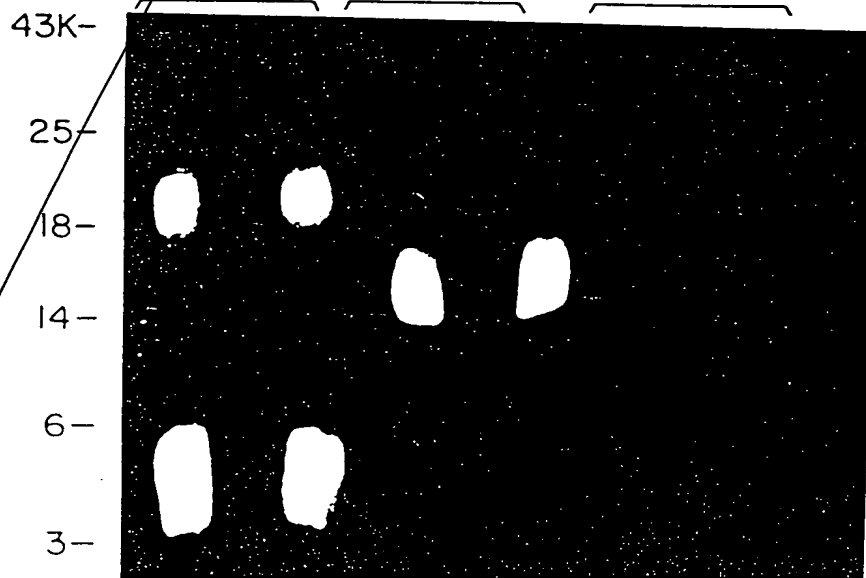
C2L	T V E D L K L N T L G R	85	90
C2S	- - - - -	- - - - -	- - - - -
PRO.	T V - A M -		

FIG. 8

d Fel-2 d Fel-4 d Fel-18 Biot 2° Ab only



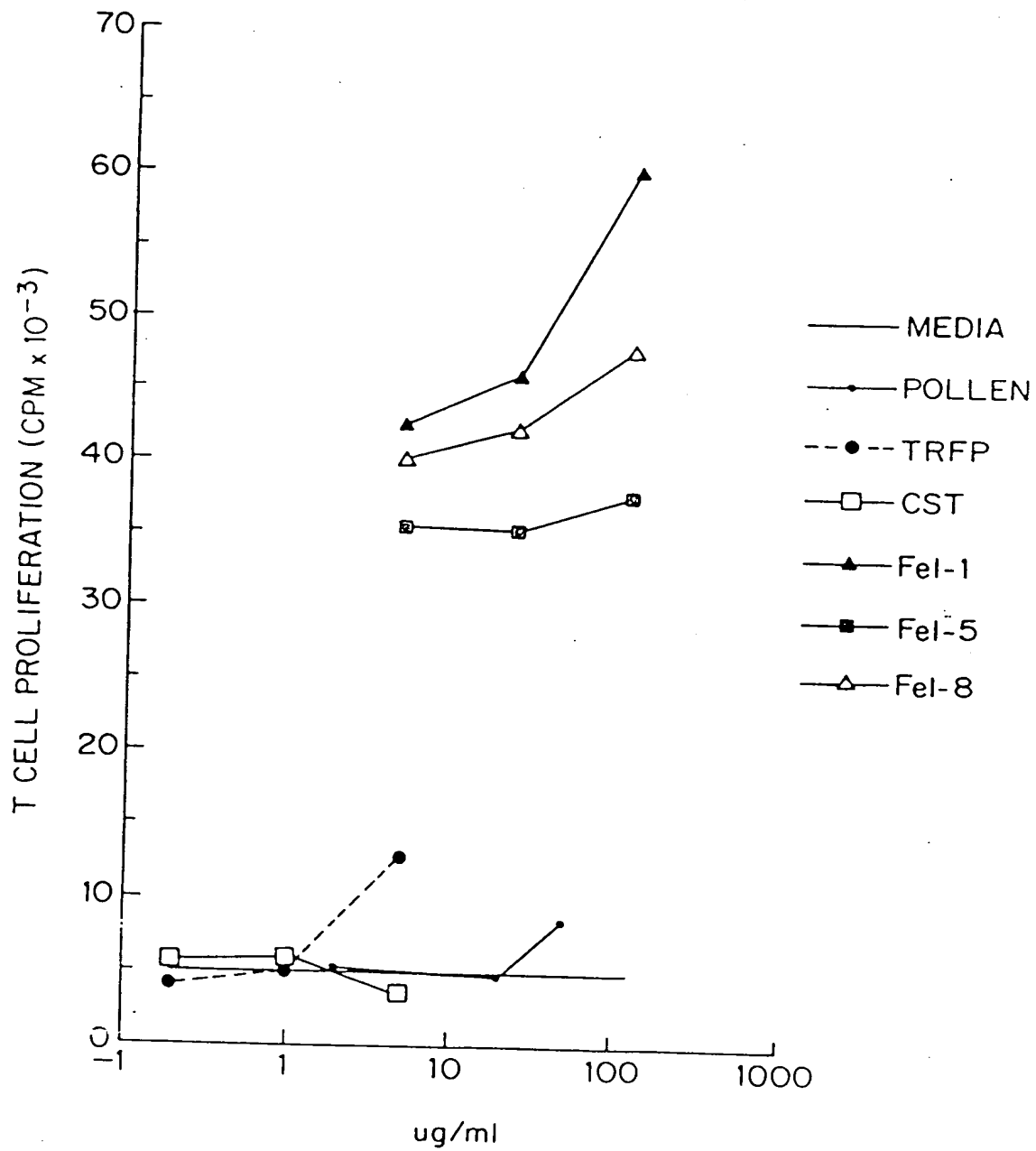
6F9
Monoclonal Antibody Human Serum JgE No first antibody control



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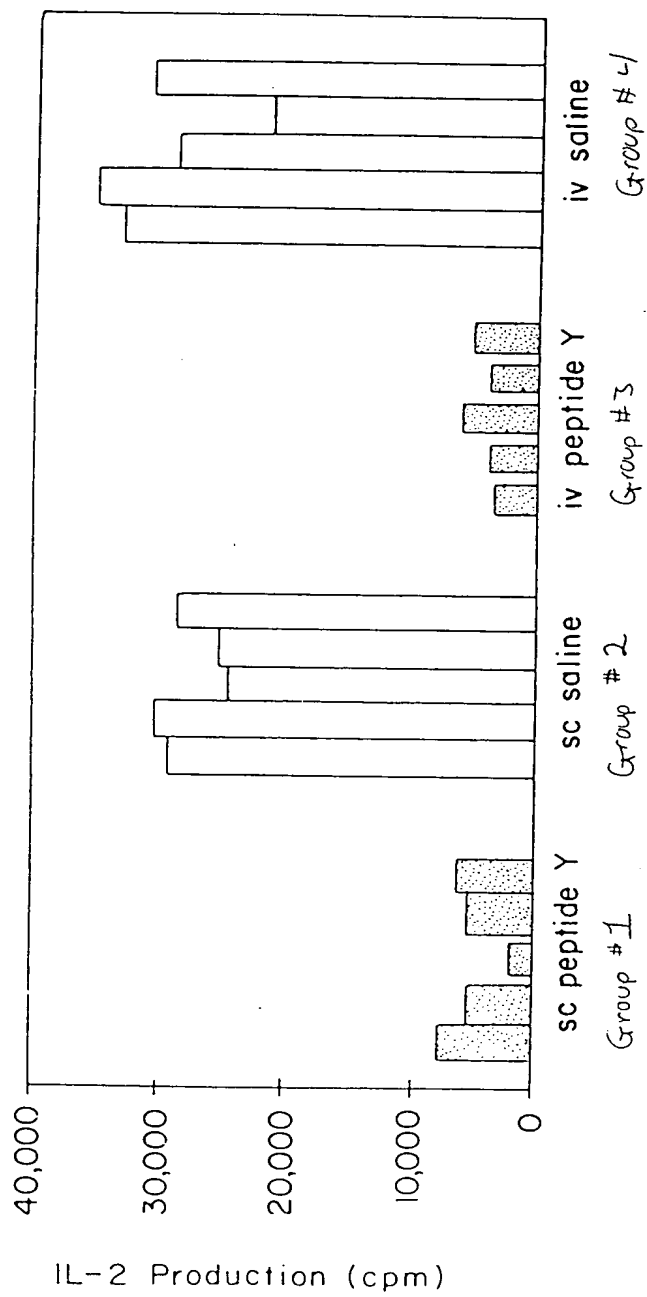
FIG. 9

PATIENT #131.2 2° (TRFP:1°)



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FIG. 10



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FIG. 11

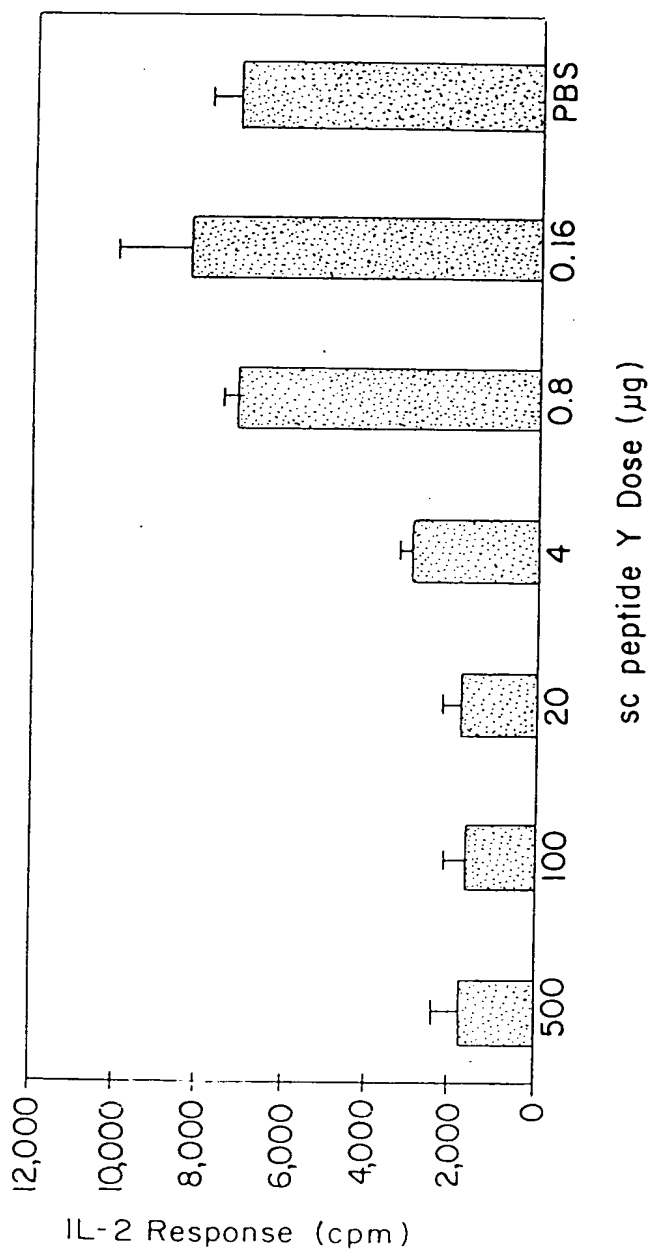


FIG. 12

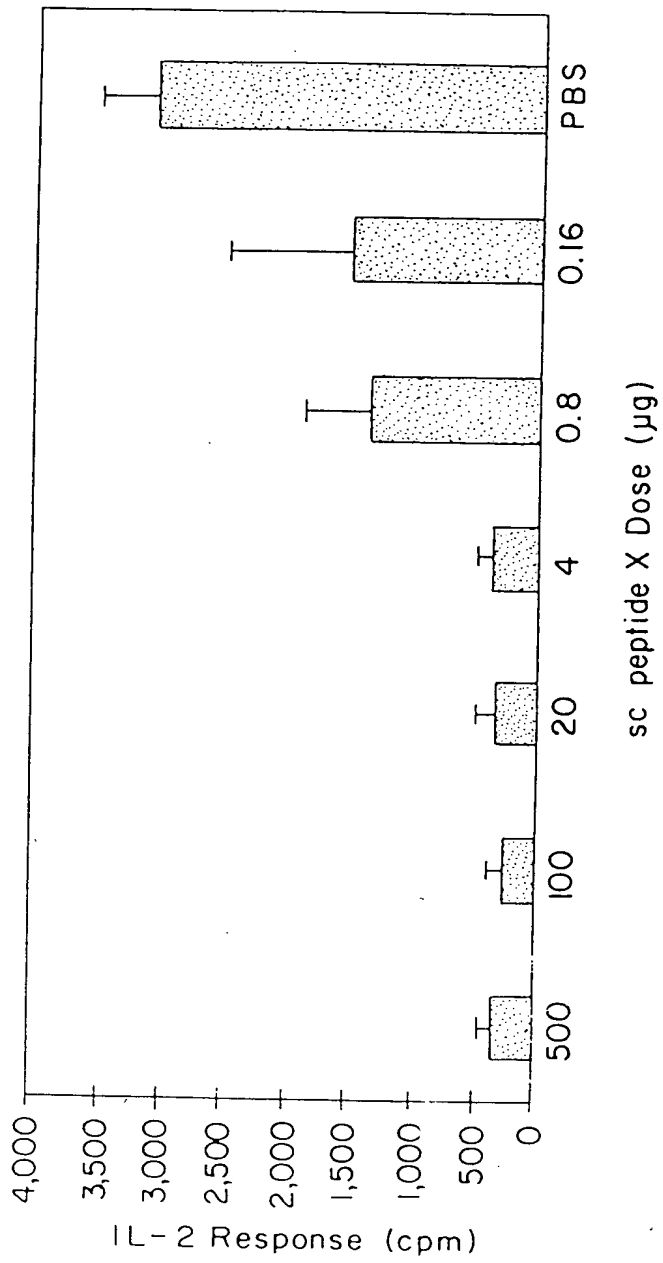
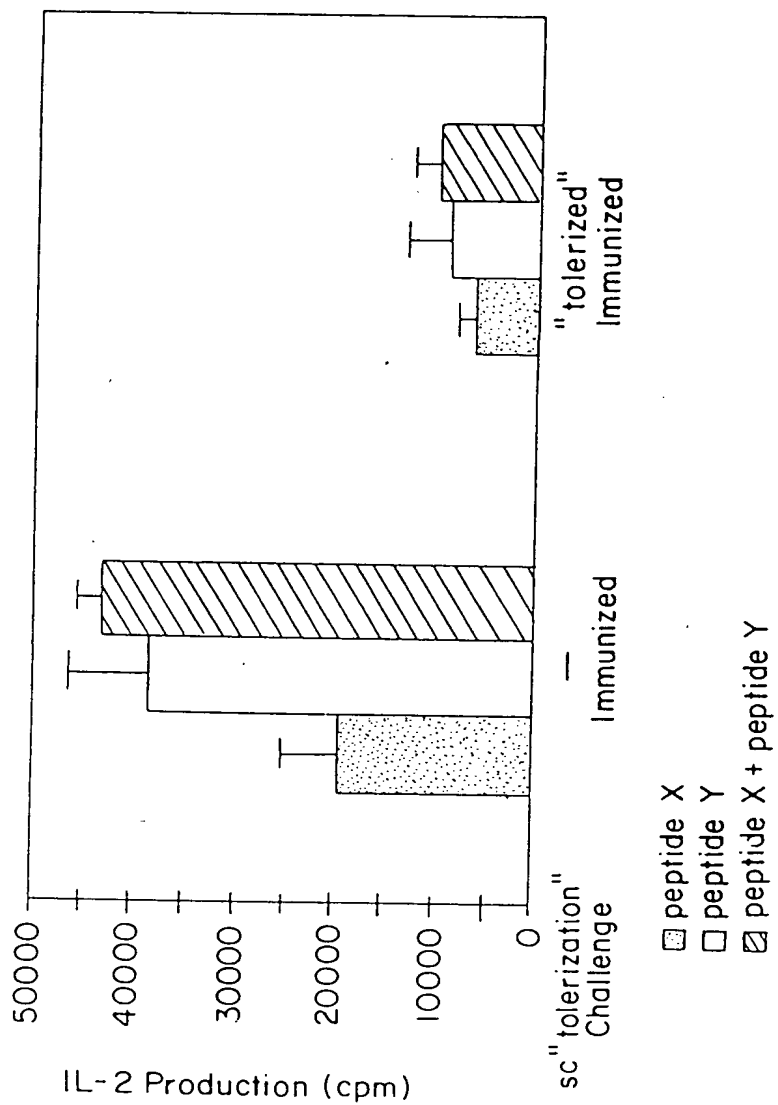


FIG. 13



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FIG. 14

LEGEND

- ▨ - Cultured with Peptide
- - Cultured without Peptide

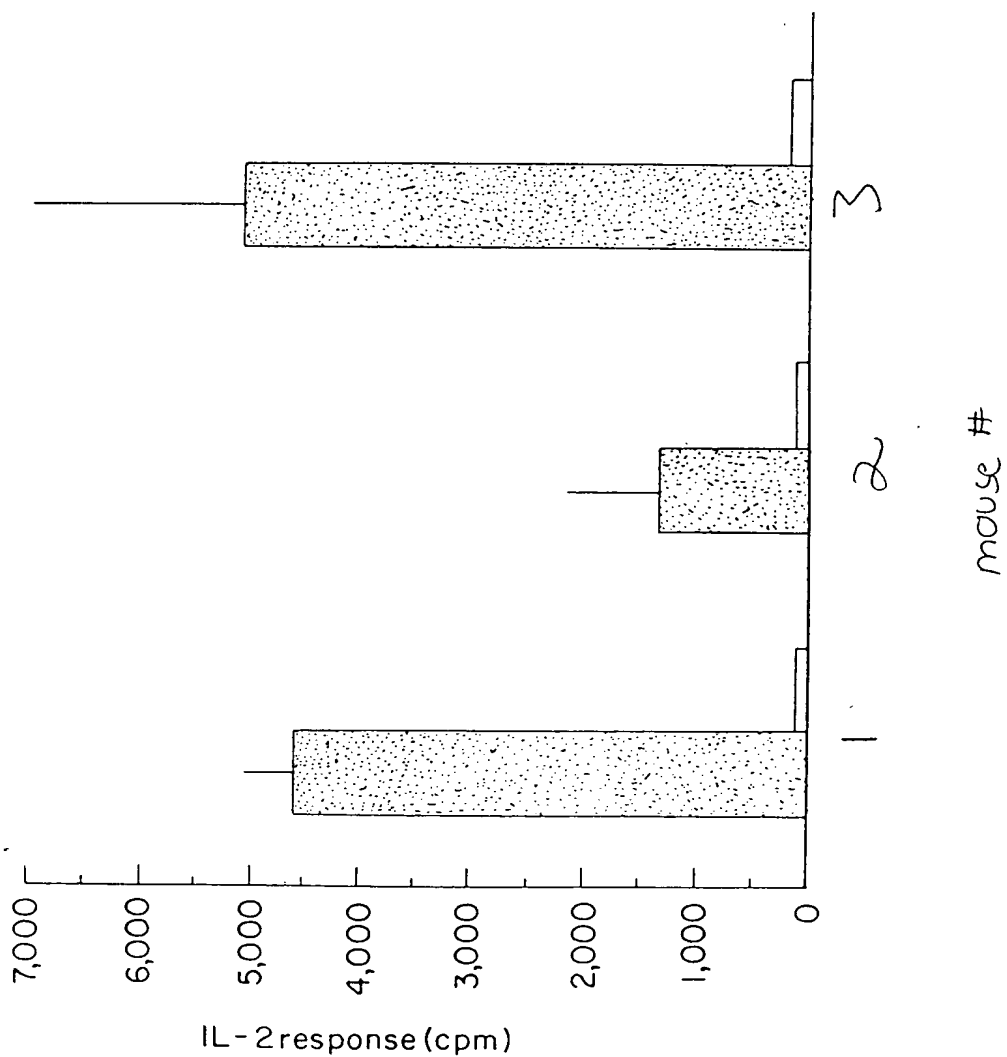


FIG. 15A & 15B

FIG. 15A

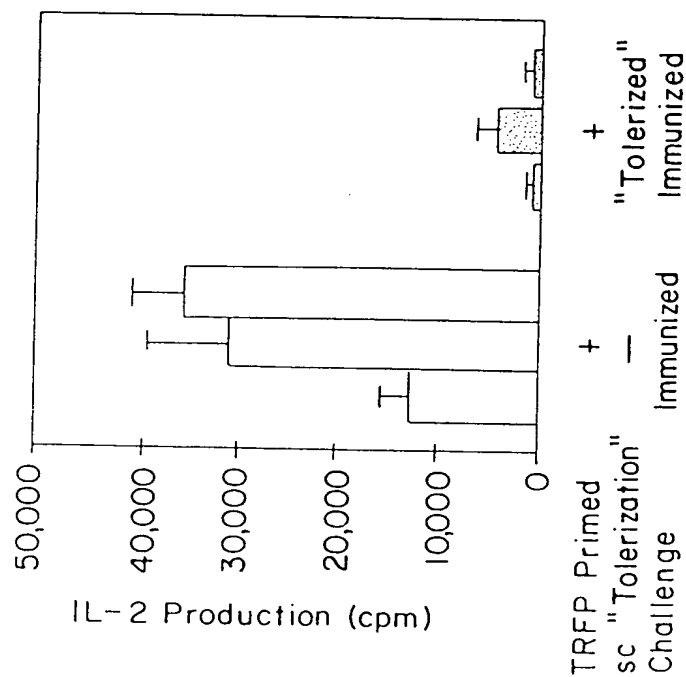


FIG. 15B

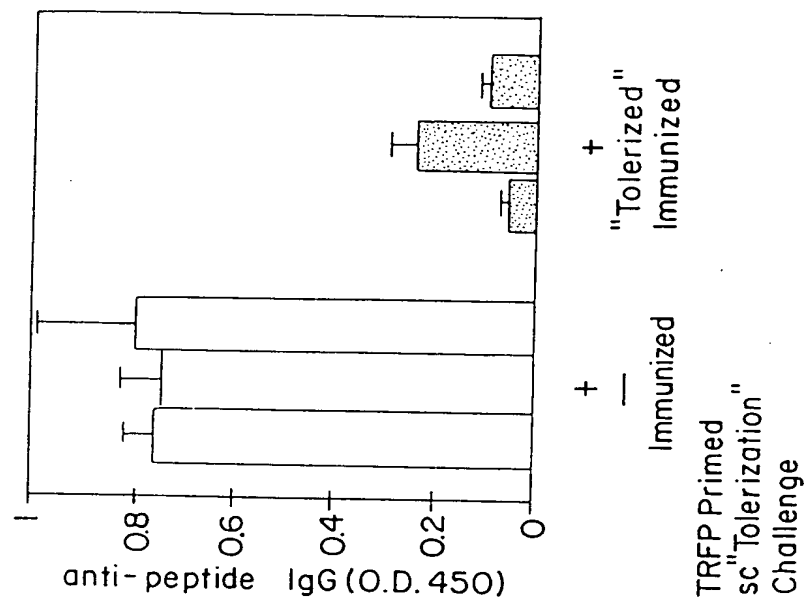


FIG. 16A & 16B

FIG. 16B

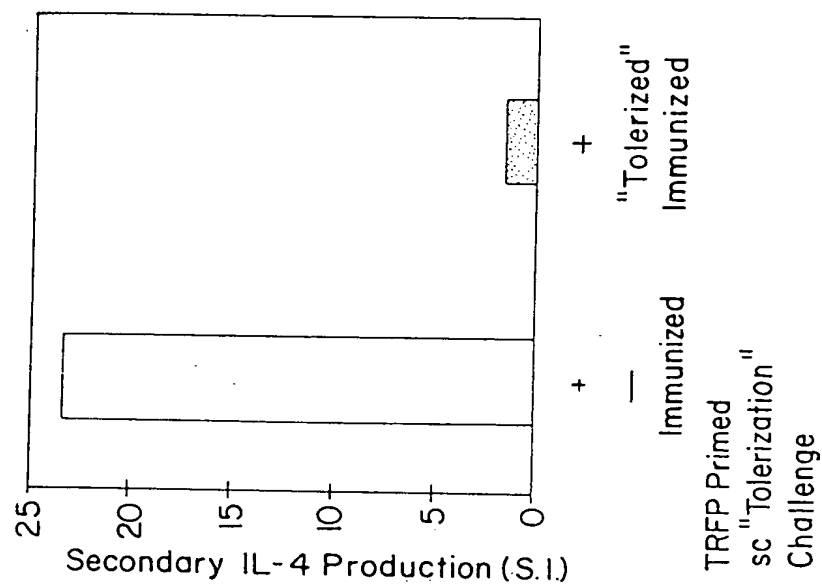


FIG. 16A

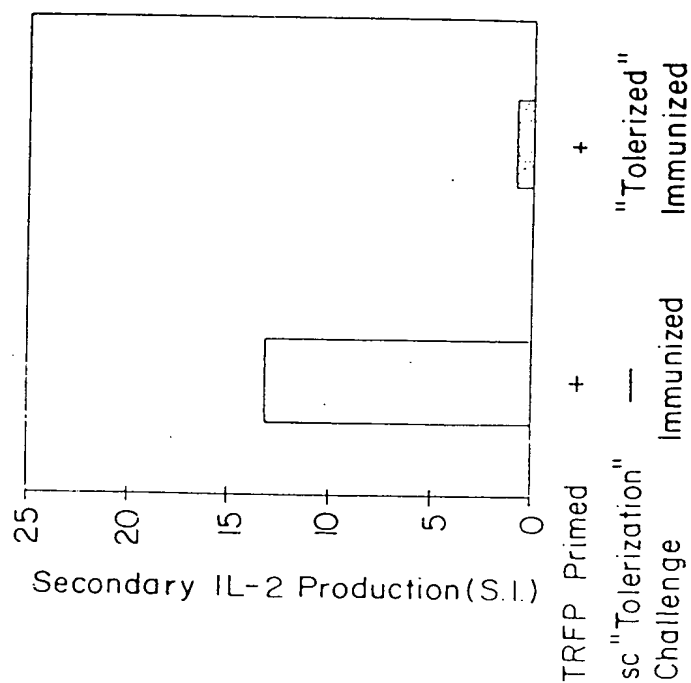


FIG. 17

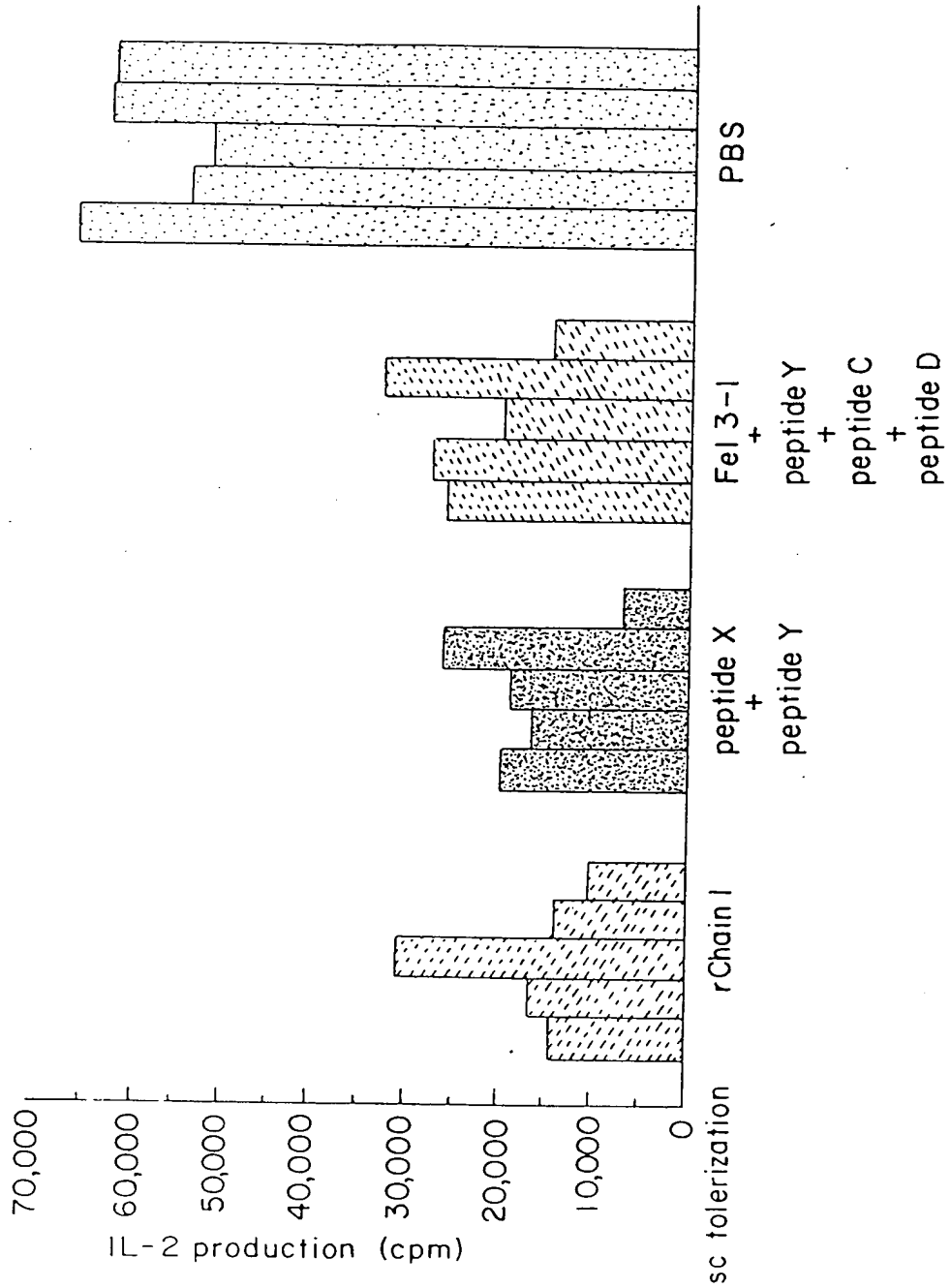


FIG. 18

Sequence

peptide
name

X	KRDVDLFLTGTPDEYVEQVAQYKALPV
Y	KALPVVLENARILKNCVDAKMTEEDKE
Z	FFAVANGNELLLDLSLTKVNPATEPER
A	EEDKENALSLLDKIYTSPL
B	MGEAVQNTVEDLKLNTLGR
C	EEDKENALSLLDKIYT
D	NALSLLDKIYTSPL

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FIG. 19

Fel 32 VKMAETCPIFYDVFFAVA
Fel 33 FYDVFFAVANGNELLLD
Fel 34 NGNELLLDLSLTKVNATE
Fel 35 SLTKVNATEPERTAMKKI
Fel 36 ERTAMKKIQDCYVENGL
Fel 37 QDCYVENGLISRVLDGLV
Fel 38 ISRVLDGLVMTTISSSKDCM
Fel 38.I ISRVLDGLVMIAINE**DCM
Fel 39 MTTISSSKDCMGEAVQNTVELDKLNTLGF
Fel 39.I MIAINE**DCMGEAVQNTVELDKLNTLGF

FIG. 20



FIG. 21

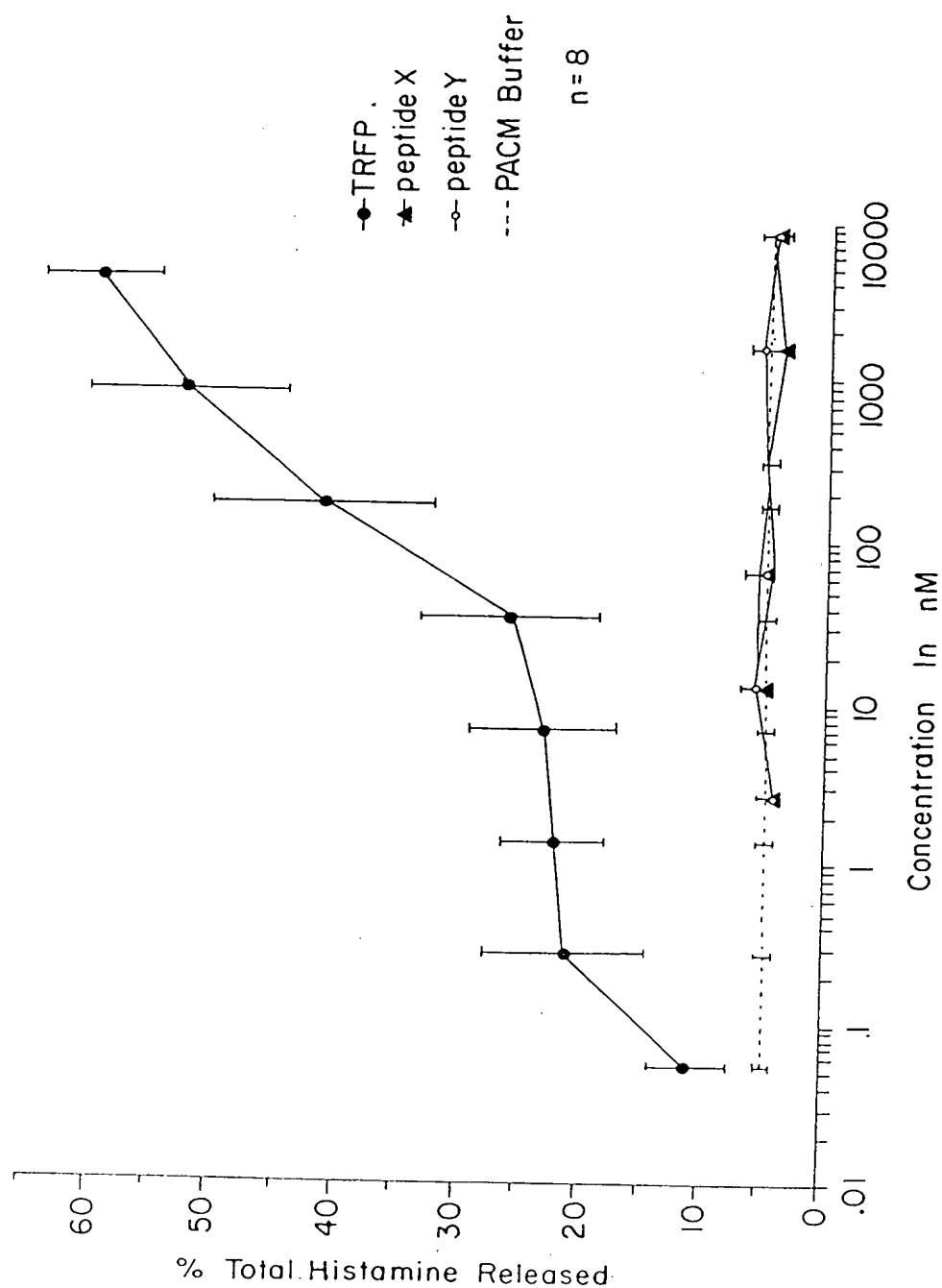


FIG. 22A

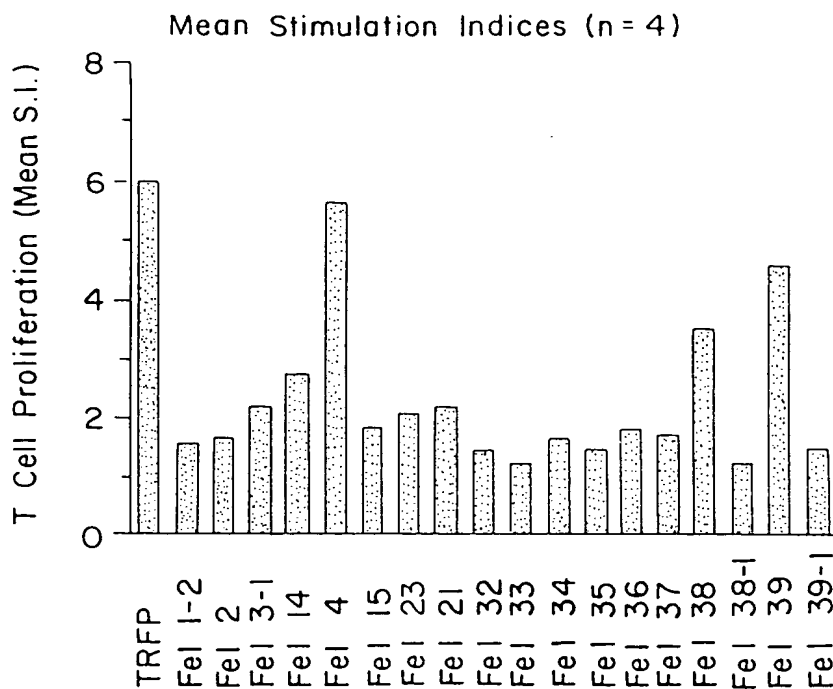


FIG. 22B

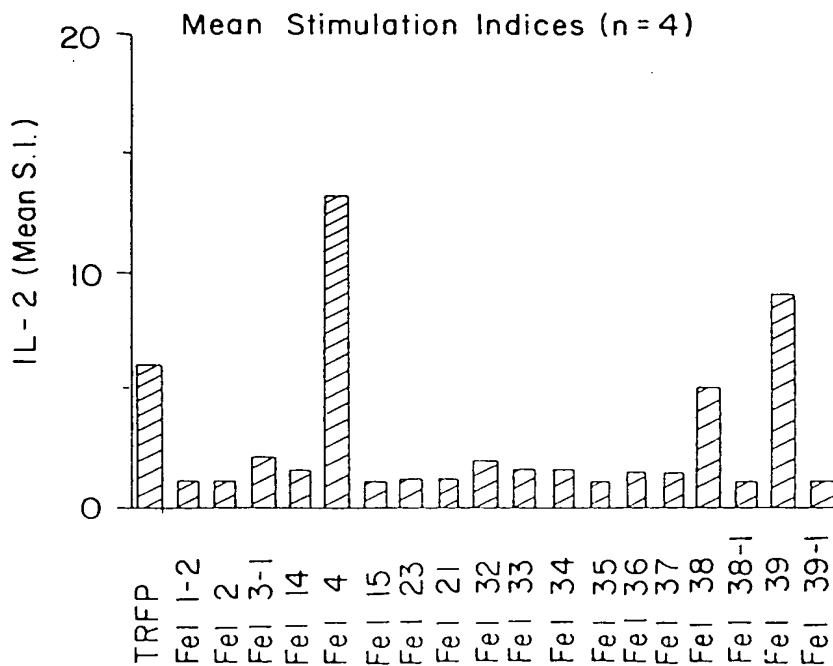


FIG. 22C

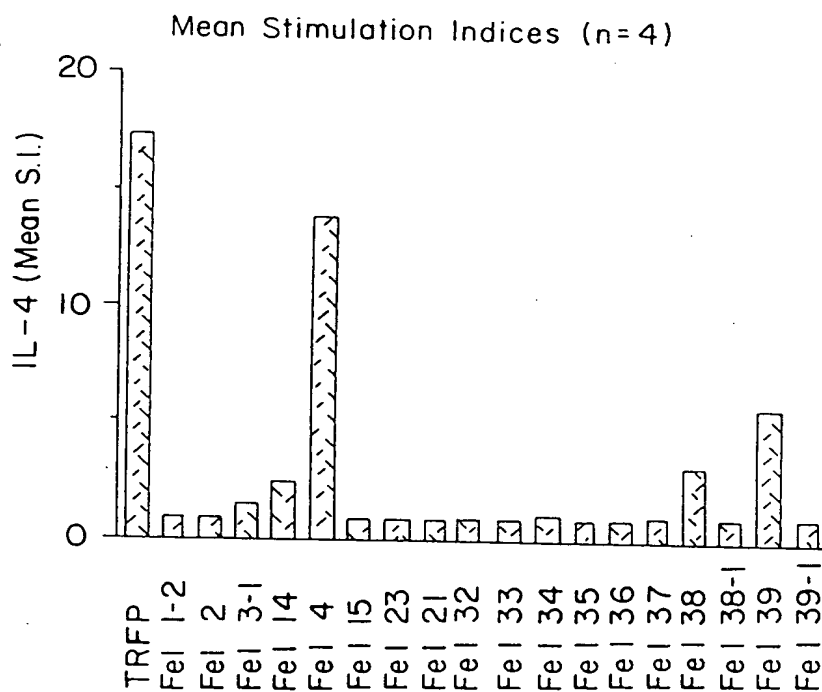


FIG. 23

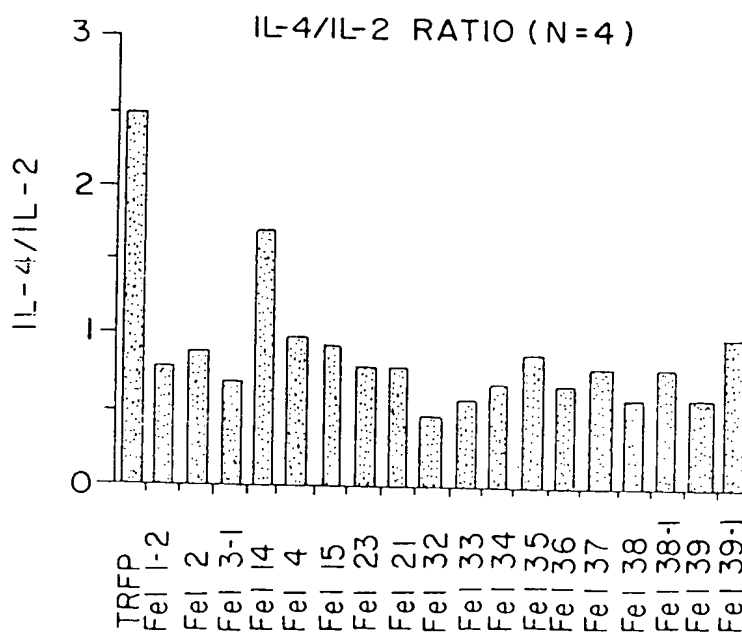
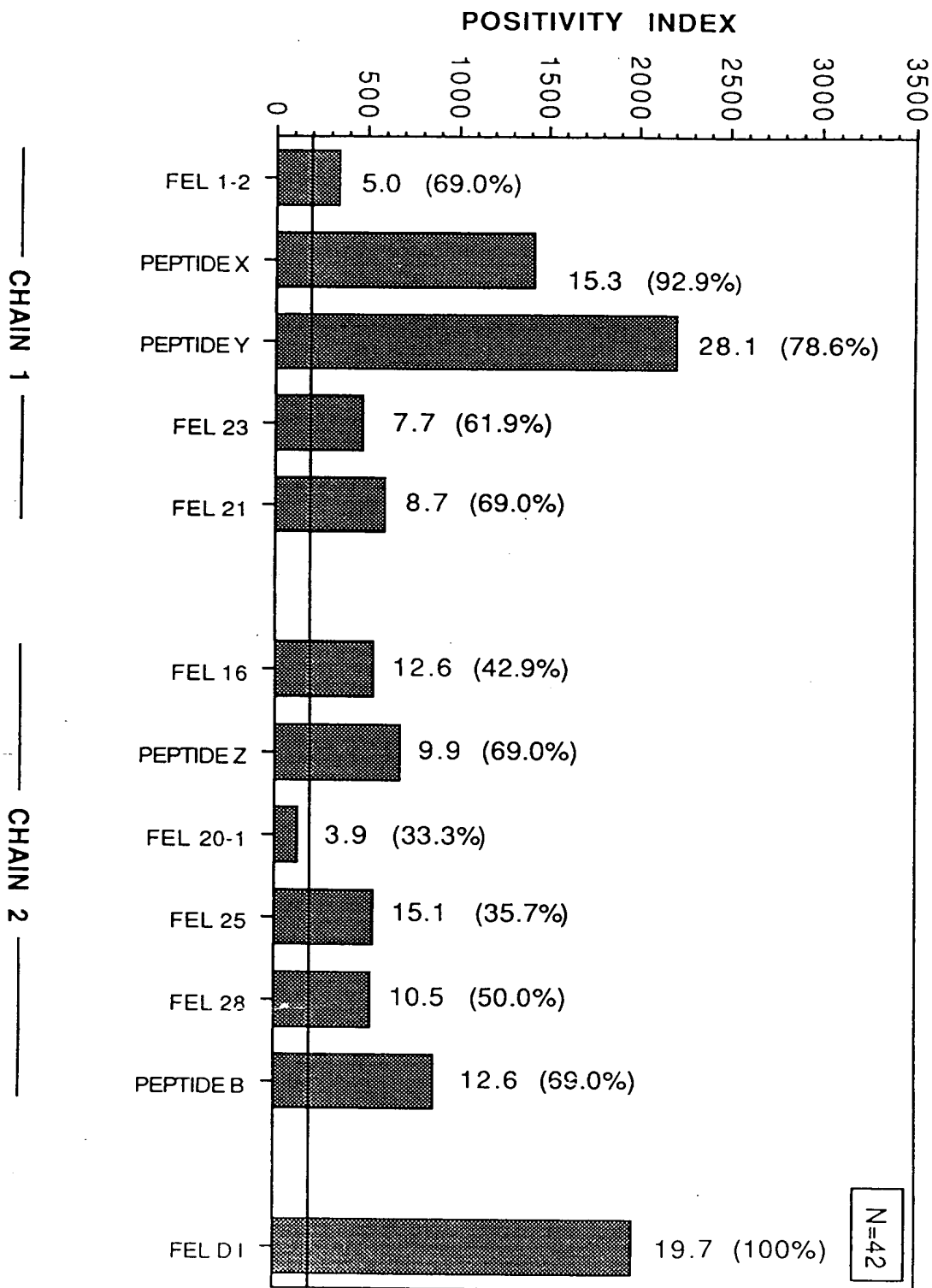


FIG. 24



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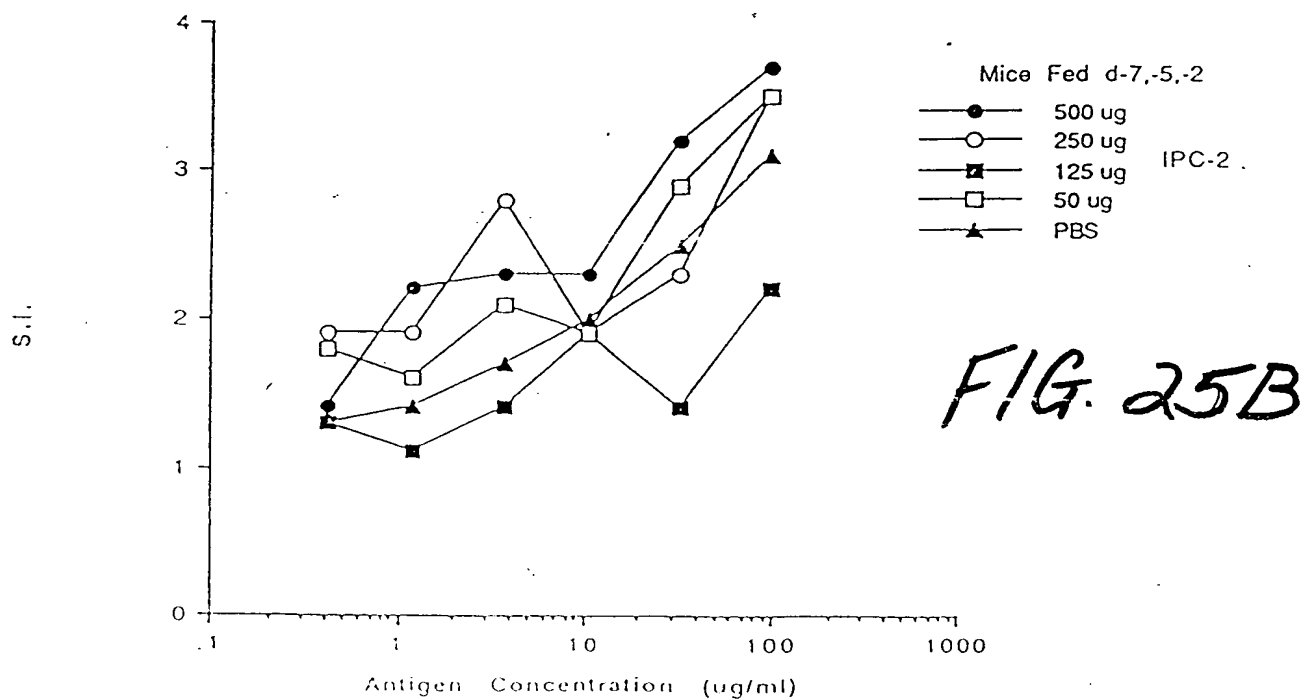
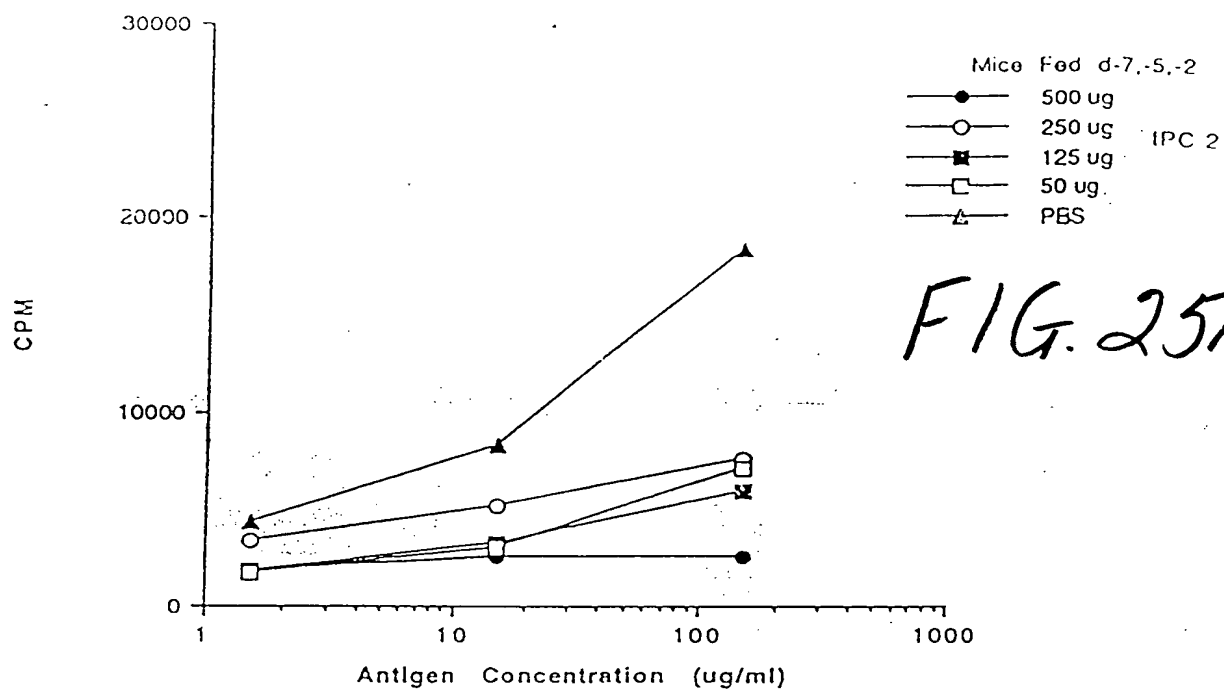


FIG. 26

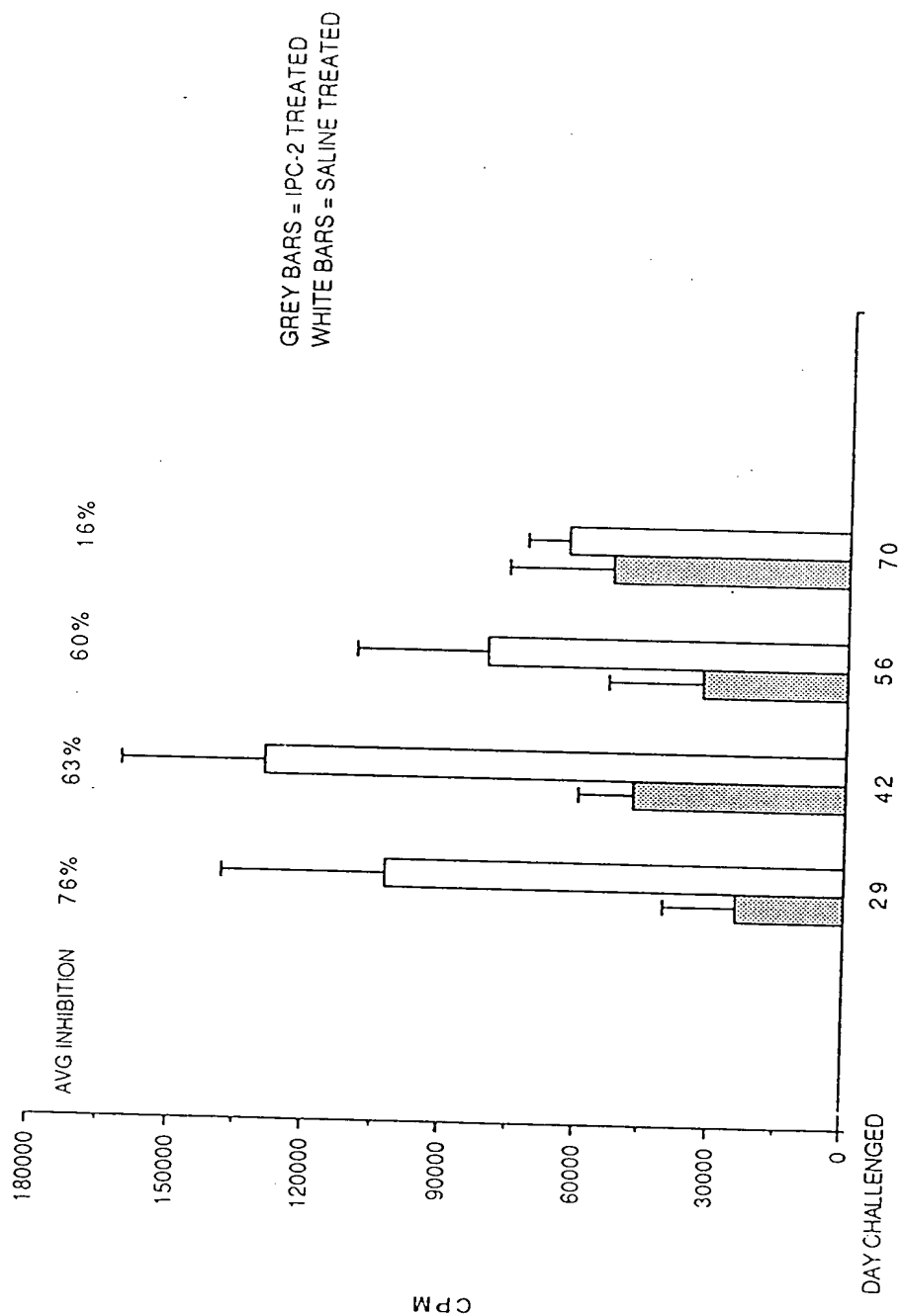


FIG. 27

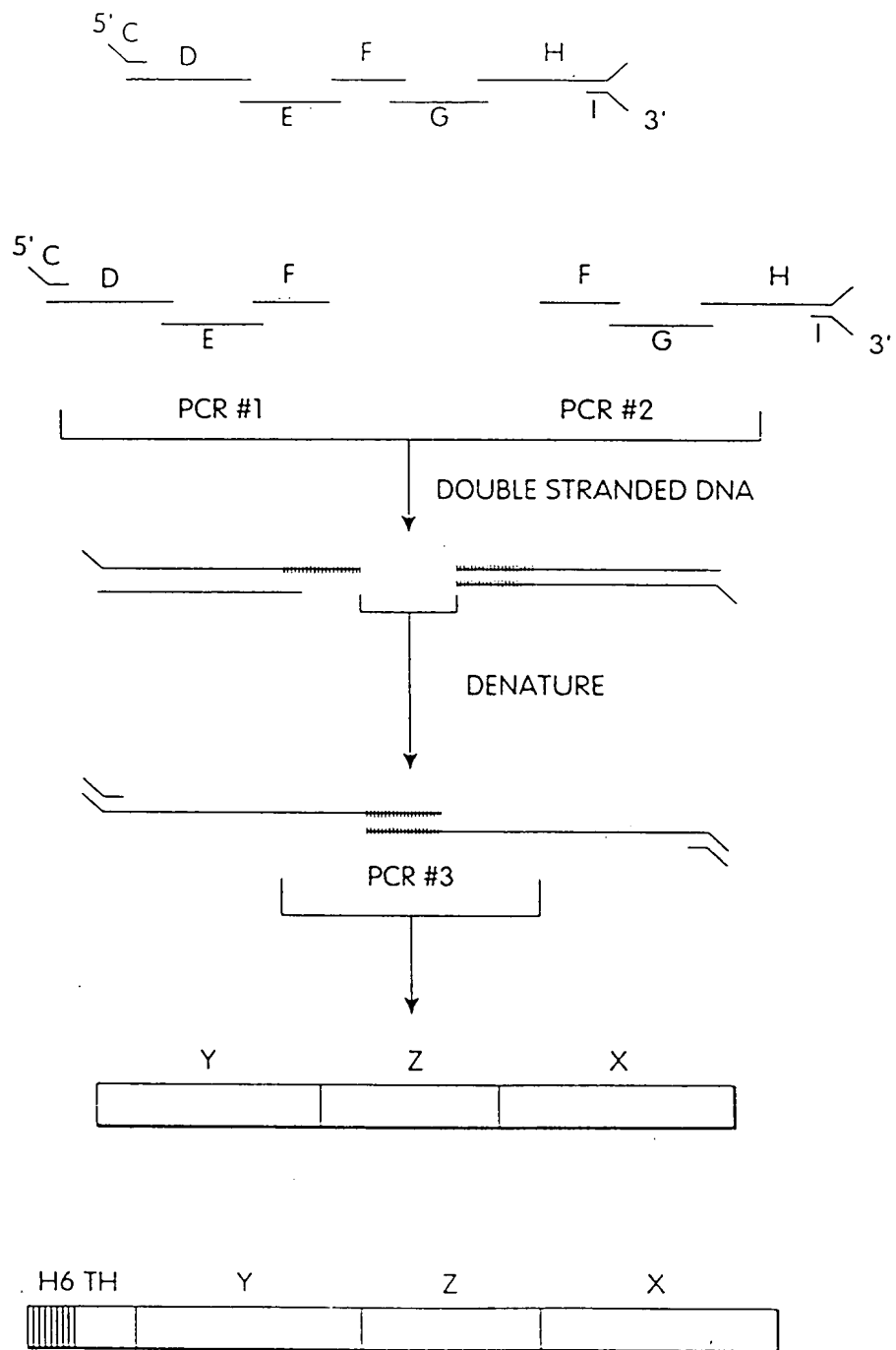
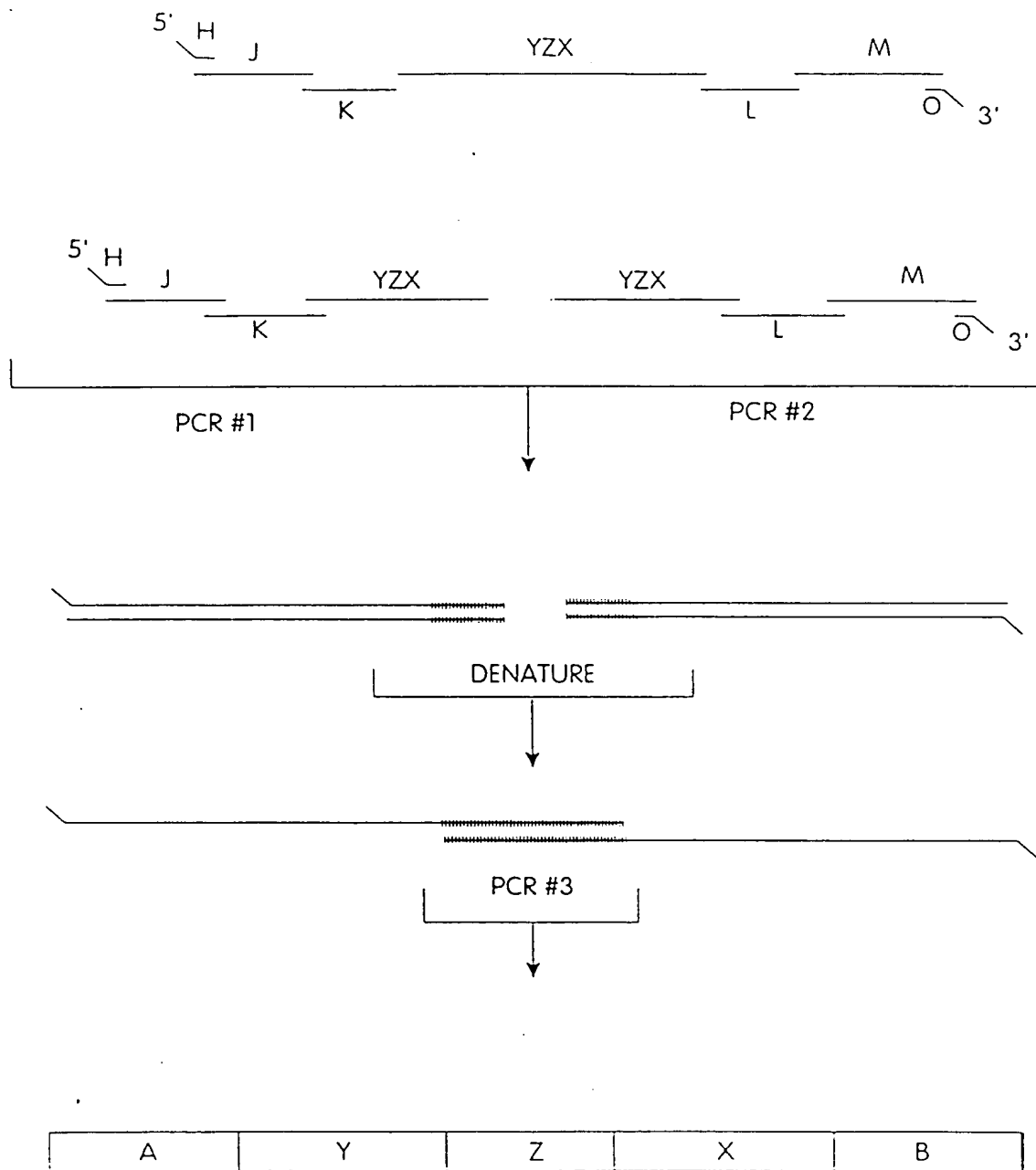


FIG. 28



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FIG. 29

C 5' BAM HI
 GGGGATCCAAAGCTCTGCCGGTGT 3'
 K A L P V V

D 5' BAM HI
 GGGGATCCAAAGCTCTGCCGGTGTCTGGAAACGCTCGTATCTGAAAACTGCGTTGACGCTAAATGACCGAA
 K A L P V V L E N A R I L K N C V D A K M T E
 GAAGACAAAGAA 3'
 E D K E

E 3' CTTCTTCTGTTTCTTAAGAAGCGACAACGATGCGCATGCTTGACGACGACCTGGACAGAGAC 5'
 E E D K E F A V A N G N E L L L D L S L

F 5' CTGGACCTGTCTCTGACCAAAAGTTAACGCTACCGAACCGGAACGT 3'
 L D L S L T K V N A T E P E R

G 3' TGGCTTGGCCCTTGCACTTGCACTGCAACTGGACAAGGACTGGCCCATGGGGCCCTG 5'
 T E P E R K R D V D L F L T G T P D

H 5' ACCGGTACCCCGGACGAATACGTTGAACAGGTTGCTCAGTACAAAGCTCTGCCGGTTAGTAGTCTAGACTGCAGAAAG
 T G T P D E Y V E Q V A Q Y K A L P V - - XBAl PSTI
 CTTGGATCCCC 3'
 HINDIII ECORI

FIG. 29 (cont.)

I 3' CGAGACGGCCAAATCATCAGATCTGACGTCTTCGAACCTAGGG 5'
A L P V - - XBAI PSTI HINDIII ECORI

J 5' GGGGATCCGAAGAAGACAAAGAAAACGGCTCTGTCTCTGCTG 3'
BAM HI E E D K E N A L S L L

K 3' GACAGAGACGACCTGTTTATAGATGTGGAGAGCGGACTTTCGAGACGGCCCAACAGACCTT 5'
L S L L D K I Y T S P L K A L P V V L E

L 3' CGAGTCATGTTTCGAGACGGCCCAATACCCACTTCGACAAGTCTTGTGGCAACTT 5'
A Q Y K A L P V M G E A V Q N T V E

M 5' CAGAACACCGTTGAAGACCTGAAACTGAACACCCCTGGGTCGTTGAATGTAACTGCAGAAATCCCC 3'
Q N T V E D L K L N T L G R - PST I ECORI

N 5' GGGGATCCGAAGAAGACAAA 3'
BAM HI E E D K

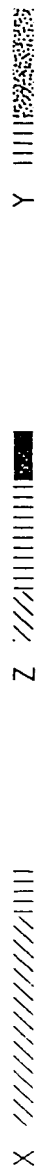
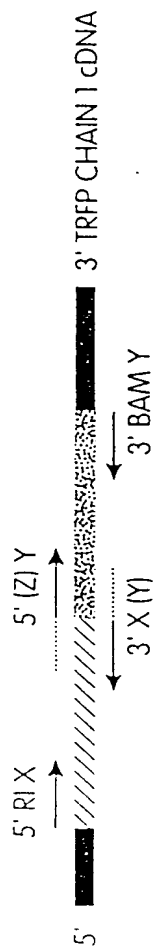
O 3' TGAACCCCTCTACTTACATTGACGTCTTAAGGG 5'
T L G R - PST I ECORI

[illegible]

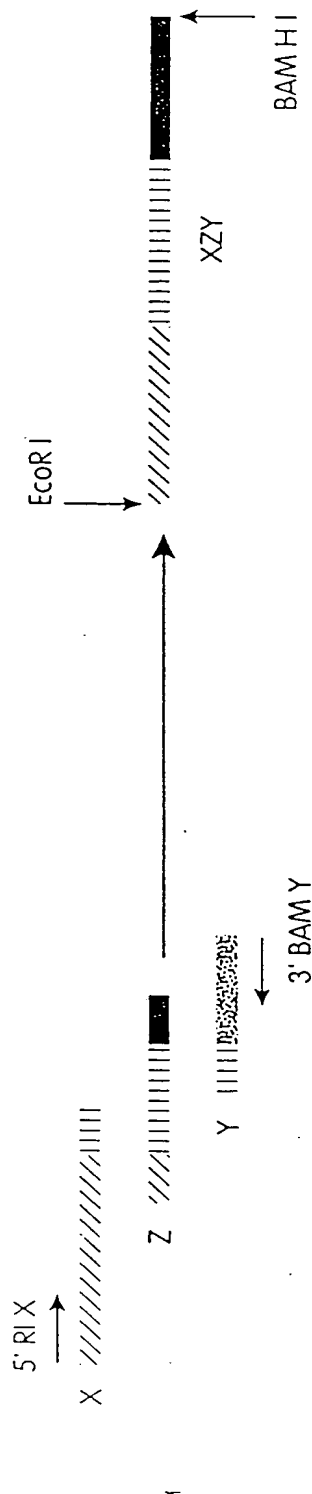
↓
ATGGGTACACCAACCAACCAACCAATTCCTGGTTCGCGTGGATCC
M G H H H H H H E F L V P R G S
AAAGCTCTGCCGTTGTCTCTGGAACGCTCGTATCCTGAAAACTGC
K A L P V V L E N A R I L K N C
GTGACGCTAAATGACCGAAGAACAAAGAAATCTTCGCTGTTGCT
V D A K M T E E D K E F F A V A
AACGGTAACGAACTGCTGCTGGACCTGTCTCTGACCAAGTTAAGCT
N G N E L L L D L S L T K V N A
ACCGAACCGAACGTAAACGTGACGTTGACCTGTTCTCCTGACCGGTACC
T E P E R K R D V D L F L T G T
CCGACGAATACGTTGAACAGGTTGCTCAGTACAAAGCTCTGCCGGTT
P D E Y V E Q V A Q Y K A L P V

FIG. 31

1) PCR INDIVIDUAL EPITOPES



2) LINK ISOLATED EPITOPES BY POOLING/PCR



[illegible]

5' PRIMERS

XZY CONSTRUCT

5' XRI 5'-GGGGAATTCAAGAGGGATGTTGACCTA-3'
ECOR I X

L P V | F F A V A N

5' (X) Z 5'-CTACCTGTATTTTTCGCGGTGGCCAAT-3'

 X Z

5' (Z) Y 5' - CCAGAGAGAAAGCACTACCTGTAGTA - 3'

P E R | K A L P V V
Z | Y

YXZ CONSTRUCT

5' YRI 5'-GGGGAATTCAAAGCACTACCTGTAGTA-3'
ECOR I Y

D K E | K R D V D L
 5' (Y) X 5' -GATAAGGAGAAGAGGGATGTTGACCTA-3'
 Y X

L P V | F F A V A N
 5' (X) Z 5' -CTACCTGTATTTTTCGCGGTGGCCAAT-3'
 X | Z

ZXY CONSTRUCT

5' ZRI 5' -GGGGAATTCTTTGCGGTGGCCAATGGA-3'

ECOR I Z

5' (Z) X 5' -AAGAGGGATGTTGACCTATTC-3' X

[illegible]

3' PRIMERS

XZY CONSTRUCT

$\alpha N \alpha A \alpha V \alpha A \alpha F \alpha F \alpha V \alpha P \alpha L \alpha A \alpha K \alpha Y$
 3' X (Z) 5' -ATTGGCCACCGCAAAAAATACAGGTAGTGCTTTGTA-3'
 $\begin{array}{c} Z \\ | \\ X \end{array}$
 $\alpha L \alpha A \alpha K \alpha R \alpha E \alpha P \alpha E \alpha T \alpha A$
 3' Z (Y) 5' -TAGTGCTTTTCTCTCTGGTTCAGTAGC-3'
 $\begin{array}{c} Y \\ | \\ Z \end{array}$
 $\alpha STOP \alpha E \alpha K \alpha D \alpha E \alpha E \alpha T$
 3' Y BAM 5' -GGGGATCCTTACTCCTTATCCTCTTCTGT-3'
 $\begin{array}{c} \text{BAMH I} \\ \hline Y \end{array}$

YXZ CONSTRUCT

```

      αL αD αV αD αR αK | αE αK αD αE αE αT
3' Y (X)  5' -TAGGTCAACATCCCTCTTCTCCTTATCCTCTTCTGT-3'
              X               | Y
      αA αF αF | αV αP αL αA αK αY
3' X (Z)  5' -CGCAAAAAATACAGGTAGTGCTTTGTA-3'
              Z |               X
      αSTOPαR αE αP αE αT αA
3' Z BAM  5' -GGGGATCCTTATCTCTCTGGTTCAGTAGC-3'
      BAMH I               Z

```

ZXY CONSTRUCT

$\alpha L \quad \alpha D \quad \alpha V \quad \alpha D \quad \alpha R \quad \alpha K$ | $\alpha R \quad \alpha E \quad \alpha P \quad \alpha E \quad \alpha T \quad \alpha A \quad \alpha N$
 3' Z (X) 5'-TAGGTCAACATCCCTCTTTCTCTCTGGTTCAGTAGCATT-3'
 X Z

 $\alpha STOP \alpha E \quad \alpha K \quad \alpha D \quad \alpha E \quad \alpha E \quad \alpha T \quad \alpha M$
 3' Y BAM 5'-GGGGATCCTCACTCCTTATCCTCTTCTGTCAT-3'
 BAMH I Y

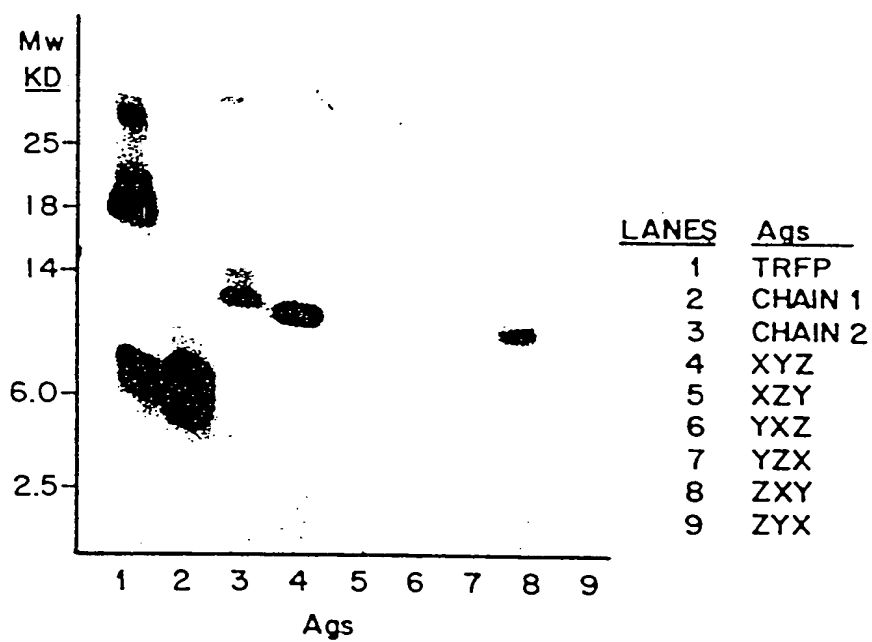
[illegible]

XZY	X	Z	Y
KRDVDL	KALPV	FFAVAN	
	FFAVAN		
	ATEPERKAL	PERKALPVV	
			TEEDKE

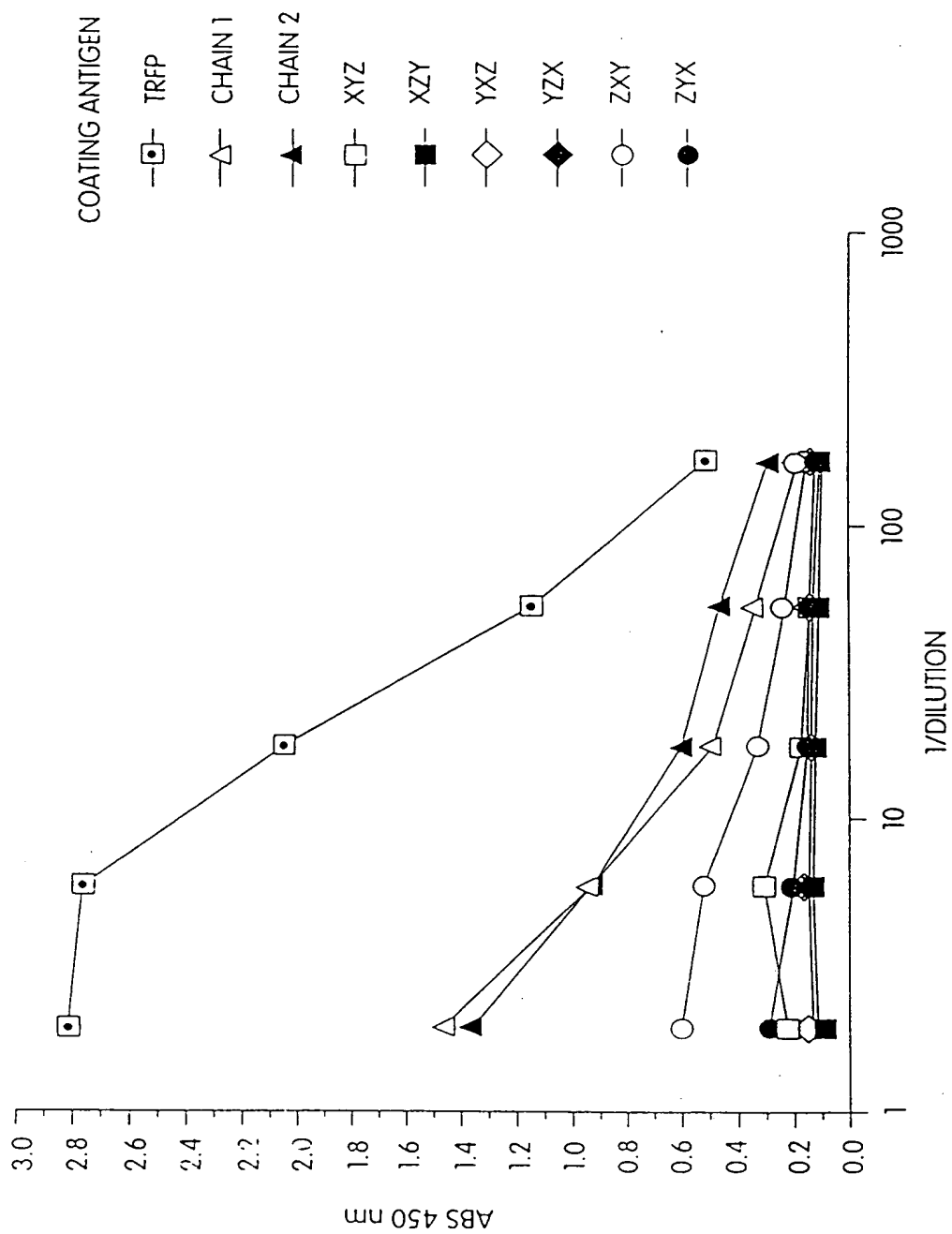
	Y	X	Z
YXX	KALPVV		
	TEEDKE	KRDVDL	
		KRDVDL	
		KALPVFFA	
		LPVFFAVAN	
			ATEPER

ZXY					
	FFAVANG				
	NATEPER	KRDVDL			
		KRDVDLP			
			QYKALPVVL		
				MTEEDKE	

FIG. 34



005160 18229960

[illegible]

005160-18229560

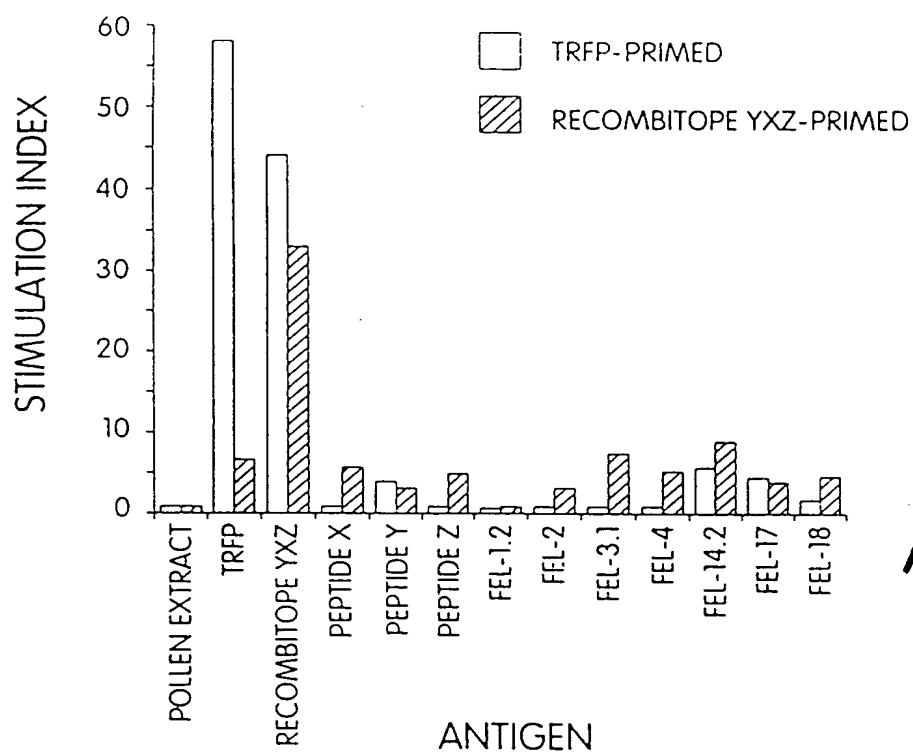


FIG. 36A

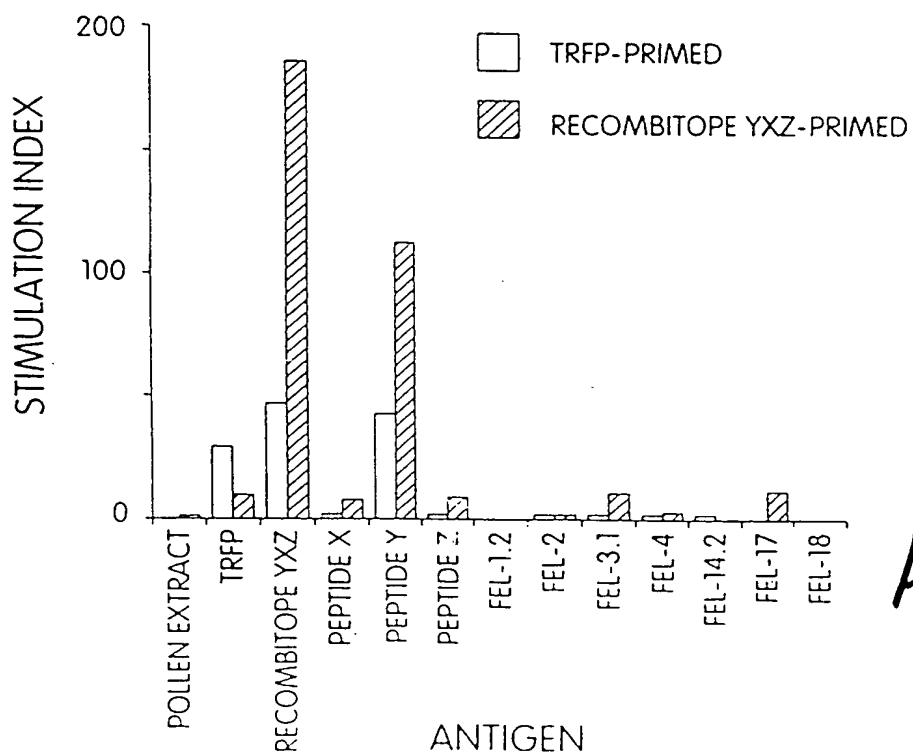


FIG. 36B

FIG. 36C

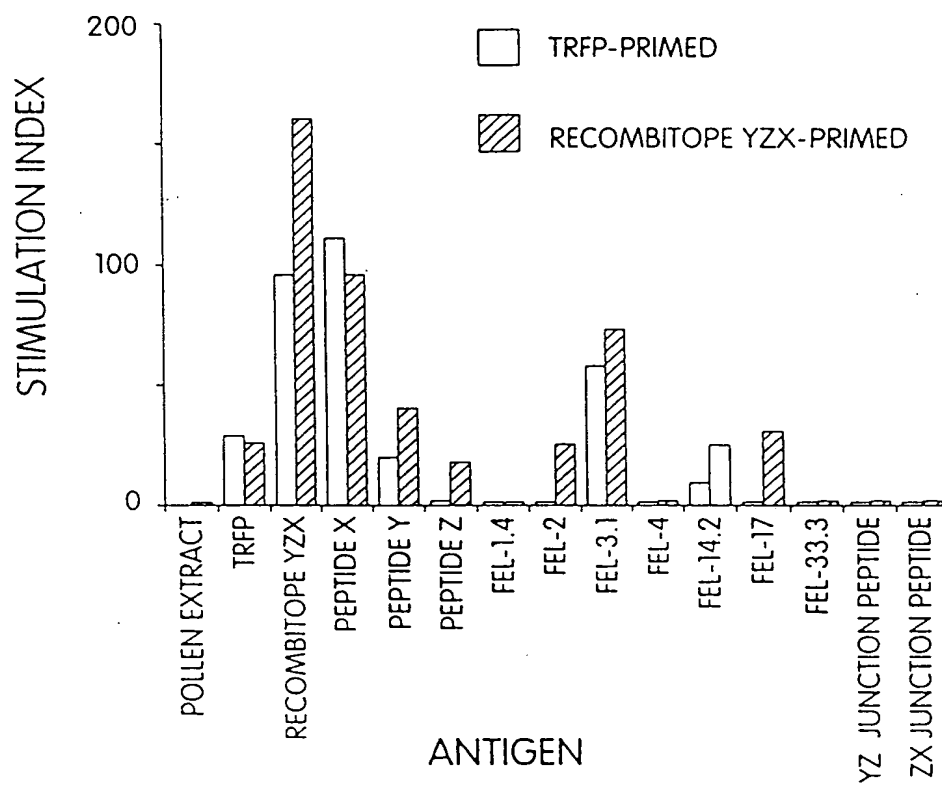


FIG. 37

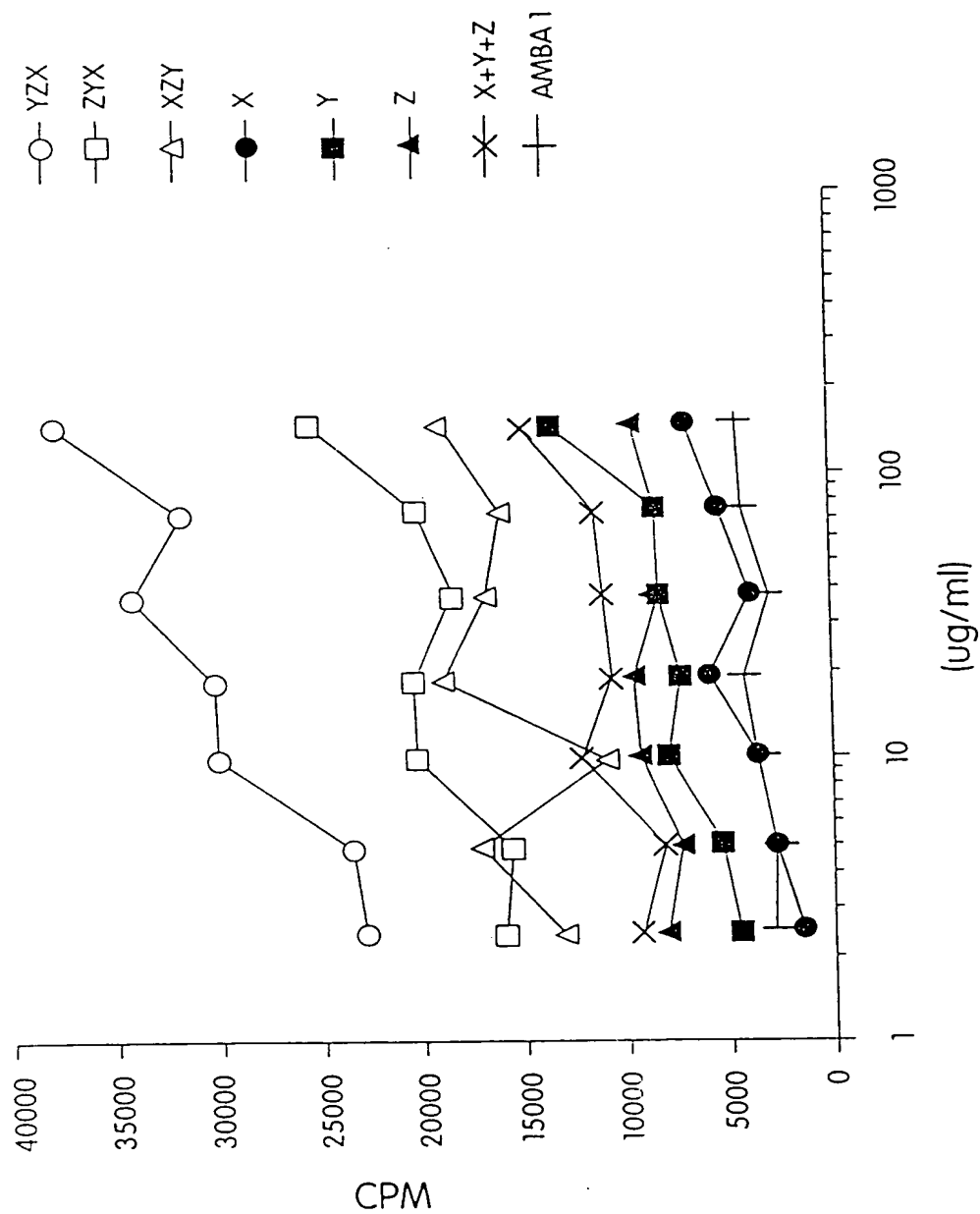
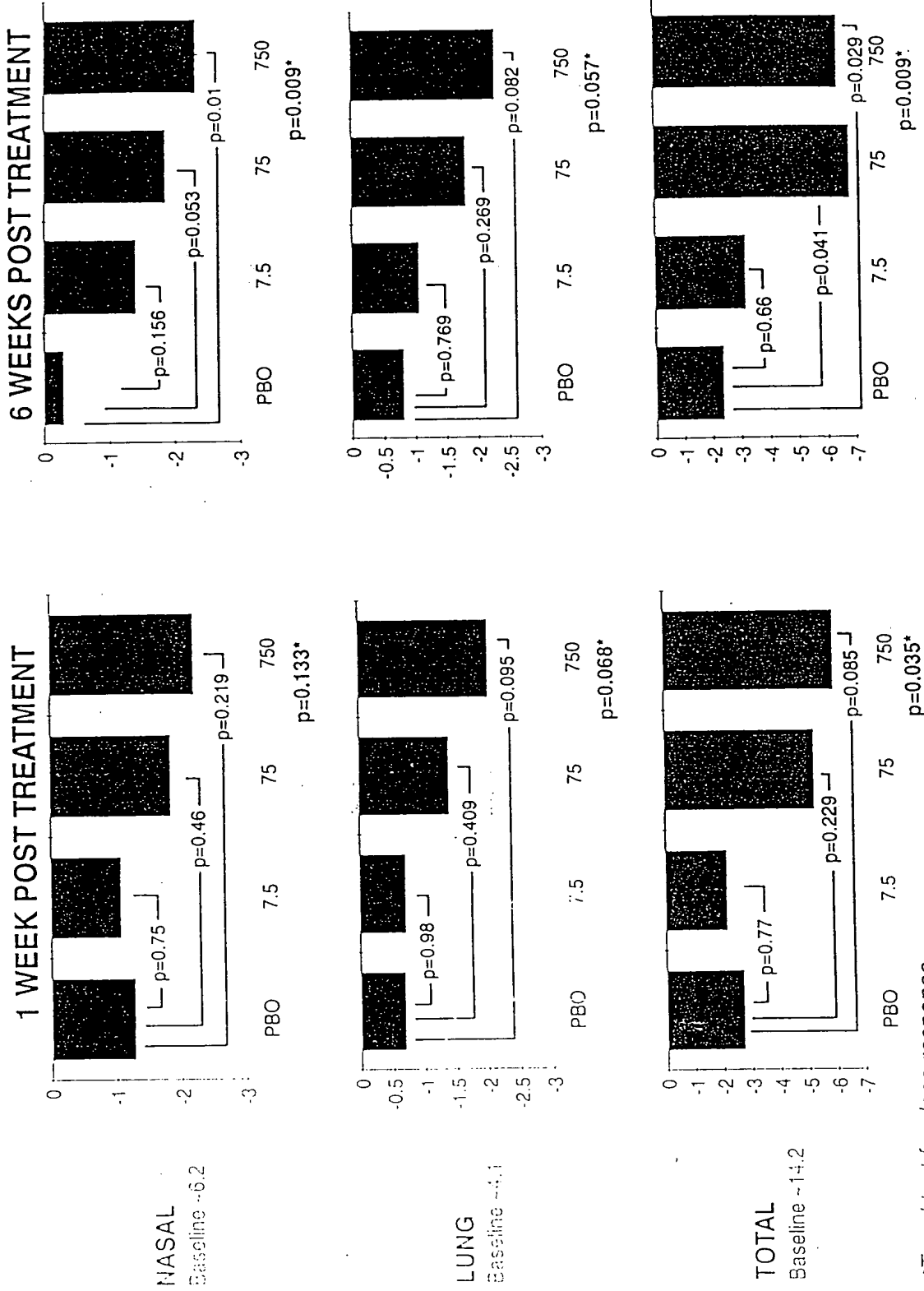


FIG. 38



*Trend test for dose response